In the specification:

Please replace Table 1 on page 40 with the following:

Table 1 *Primers and boundary sequences of PTCH*

Exon	5' Boundary[a]	Nucleotide Position[b]	Exon Size	3' boundary[a]	Reading Frame[c]	Primers	
1	ND[d]	ND	ND	AAG|gtgnat	ND		
2	ND	202	193	AAG|gtaaga	3		
3	tgtcag|T	395	190	CAG|gtaagg	1	3F	GAGTTTGCAGTGATGTTGCTATTC (SEQ ID NO: 23)
						3R	ACCGCCTTACCTGCTGCTC (SEQ ID NO: 24)
4	tattag|G	585	70	CAG|gtatat	2	4F	TGCACTAATTTTCTTATTACAGTGAG (SEQ ID NO: 25)
						4R	TAAGGCACACTACTGGGGTG (SEQ ID NO: 26)
5	tgacag|A	655	92	CCT|gtaagt	3	5F	GAACACCCCAGTAGTGTGCC (SEQ ID NO: 27)
						5R	TGAGTCCTAGAGAAGTCACAGACATC (SEQ ID NO: 28)
6	ttgcag|A	747	199	AAA|gtgagt	2	6F	GGCTCTTTTCATGGTCTCGTC (SEQ ID NO: 29)
						6R	TGTTTTGCTCTCCACCCTTC (SEQ ID NO: 30)
7	ttttag|C	946	122	CAG|gtaagc	3	7F	GCACTGGATTTTAACAAGGCATG (SEQ ID NO: 31)
						7R	AGGGCATAGATTGTCCTCGG (SEQ ID NO: 32)
8	ctgcag|C	1068	148	GAG|gtaaac	2	8F	TGGGAATACTGATGATGTGCC (SEQ ID NO: 33)
						8R	CATAACCAGCGAGTCTGCAC (SEQ ID NO: 34)
9	ccacag|G	1216	132	ATG|gtaacg	3	9F	CATTTGGGCATTTCGCATTC (SEQ ID NO: 35)
						9R	ACCAAACCAAACTCCAGCCC (SEQ ID NO: 36)
10	ttgcag|C	1348	156	CAG|gtacta3	3	10F	TGCCCCCATTGTTCTGCTTG (SEQ ID NO: 37)
						10R	GGACAGCAGATAAATGGCTCC (SEQ ID NO: 38)
11	ctgtag|G	1504	99	GAG|gtaatg	3	11F	GCATCTCGCATGTCTAATGCCAC (SEQ ID NO: 39)
						11R	AAGCTGTGATGTCCCCAAAG (SEQ ID NO: 40)
12	tcccag|G	1603	126	CAG|gtgagc	3	12F	GACCATGTCCAGTGCAGCTC (SEQ ID NO: 41)
						12R	CGTTCAGGATCACCACAGCC (SEQ ID NO: 42)
13	tcccag|G	1729	119	AAG|gtacat	3	13F	AGTCCTCTGATTGGGCGGAG (SEQ ID NO: 43)
						13R	CCATTCTGCACCCAATCAAAAG (SEQ ID NO: 44)
14	tttcag|C	1848	403	AAG|gtaatc	2	14F	AAAATGGCAGAATGAAAGCACC (SEQ ID NO: 45)
						14R	CTGATGAACTCCAAAGGTTCTG (SEQ ID NO: 46)
15	ttccag|G	2251	310	AGG|gtaaga	3	15F	GGAAGAGTCAGTGGTGCTCC (SEQ ID NO: 47)
						15R	CGCCAAAGACCGAAAGGAC (SEQ ID NO: 48)
16	ttctag|G	2561	143	CAG|gtactc	1	16F	AGGGTCCTTCTGGCTGCGAG (SEQ ID NO: 49)
						16R	GCTGTCAAGCAGCCTCCAC (SEQ ID NO: 50)
17	ttgtag|T	2704	184	GAA|gtaagt	3	17F	GCTCTCAAGGCAGAAGTGTG (SEQ ID NO: 51)
						17R	GGAAGGCACCTCTGTAAGTTC (SEQ ID NO: 52)
18	gtccag|T	2888	281	ATT|gtgagt	1	18F	GCTCCTAACCTGTGCCCTTC (SEQ ID NO: 53)
						18R	GAATTTGACTTCCACAAAGCCC (SEQ ID NO: 54)
19	ctccag|G	3169	138	TTG|gtatgg	3	19F	CGCCCACTGACCACTGTGTG (SEQ ID NO: 55)
						19R	GAGCCAGAGGAAATGGGTTG (SEQ ID

Table 1 *Primers and boundary sequences of PTCH*								
Exon	5' Boundary[a]	Nucleotide Position[b]		Exon Size		3' boundary[a]	Reading Frame[c]	Primers
								NO: 56)
20	gcacag|G	3307		143		CAG|gtaagc	3	20F AGCATTTACCAGGTGAAGTCC (SEQ ID NO: 57)
								20R TTGCACACGCCTGCTTAC (SEQ ID NO: 58)
21	tcccag|G	3450		100		GAG|gtcagt	2	21F TGTTCCCGTTTCCTCTTG (SEQ ID NO: 59)
								21R GCACAGGAAACACAGCATTC (SEQ ID NO: 60)
22	aaatag|G	3550		255		ACT|gtaagt	3	22F GCAGGTAAATGGACAAGAACAC (SEQ ID NO: 61)
								22R ACTACCACGGTGGGAAGACC (SEQ ID NO: 62)
23	ctgcag|G	3805		541		GAG/gtgagt	3	23F CCCTTCTAACCCACCCTCAC (SEQ ID NO: 63)
								23R GACACATCAGCCTTGCTC (SEQ ID NO: 64)
24	ND	4346		ND		ND		

[a] Consensus sequences for the 5' and 3' exonic boundaries are $(t/c)_{11}$ncag|G and AG|gt$^{g}_{a}$agt, respectively (20). Upper case denotes exonic sequence.
[b] Exon positions are in reference to the coding sequence of *PTCH* (3) with the beginning ATG as nucleotide 1.
[c] 5' exon boundary begins after the first, second, or third base of the codon of the translation reading frame.
[d] ND, not determined.